ALIGNMENT 1: SEQ ID NO:7

```
                   1                    30 31                   60 61                   90 91                  120
Original_Seq7      GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Substitute_Seq7    GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Amended_Seq7       GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC
Original_Fig4      GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC

                   121                  150 151                  180 181                  210 211                  240
Original_Seq7      GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Substitute_Seq7    GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Amended_Seq7       GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT
Original_Fig4      GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT

                   241                  270 271                  300 301                  330 331                  360
Original_Seq7      TCCTTCTGGATTCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Substitute_Seq7    TCCTTCTGGATCCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Amended_Seq7       TCCTTCTGGATTCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT
Original_Fig4      TCCTTCTGGATTCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCGCGGT

                   361                  390 391                  420 421                  450 451                  480
Original_Seq7      AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Substitute_Seq7    AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Amended_Seq7       AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Original_Fig4      AACCGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC

                   481                  510 511                  540 541                  570 571                  600
Original_Seq7      AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Substitute_Seq7    AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Amended_Seq7       AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Original_Fig4      AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC

                   601                  630 631                  660 661                  690 691                  720
Original_Seq7      GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Substitute_Seq7    GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Amended_Seq7       GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG
Original_Fig4      GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG

                   721                  750 751                  780 781                  810 811                  840
Original_Seq7      GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Substitute_Seq7    GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Amended_Seq7       GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC
Original_Fig4      GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC

                   841                  870 871                  900 901                  930 931                  960
Original_Seq7      CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Substitute_Seq7    CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Amended_Seq7       CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC
Original_Fig4      CAGAACTCTAAATACATCAACTACCGCGAC CTGTACATCGGTGAAAAGTTCATCATCCGT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC

                   961                  990 991                  1020 1021                 1050 1051                 1080
Original_Seq7      CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Substitute_Seq7    CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Amended_Seq7       CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC
Original_Fig4      CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAGAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACCATC

                   1081                 1110 1111                 1140 1141                 1170 1171                 1200
Original_Seq7      CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Substitute_Seq7    CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Amended_Seq7       CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC
Original_Fig4      CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC GGTATCCACCGTTTCTACGAATCTGGTATC

                   1201                 1230 1231                 1260 1261                 1290 1291                 1320
Original_Seq7      GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Substitute_Seq7    GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Amended_Seq7       GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT
Original_Fig4      GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAAGACGAAGGT

                   1321        1341
Original_Seq7      TGGACCGAATAGTAAGAATTC
Substitute_Seq7    TGGACCGAATAGTAAGAATTC
Amended_Seq7       TGGACCGAATAGTAAGAATTC
Original_Fig4      TGGACCGAATAGTAAGAATTC
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ALIGNMENT 2: SEQ ID NO:37

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              1                 30 31                60 61                90 91               120
Original_Seq37   CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Substitute_Seq37 CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Amended_Seq37    CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT
Fig2_'975_App    CTCGAGCCATGGCTCGTCTGCTGTCTACCT TCACTGAATACATCAAGAACATCATCAATA CCTCCATCCTGAACCTGCGCTACGAATCCA ATCACCTGATCGACCTGTCTCGCTACGCTT

              121               150 151               180 181               210 211              240
Original_Seq37   CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Substitute_Seq37 CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Amended_Seq37    CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT
Fig2_'975_App    CCAAAATCAACATCGGTTCTAAAGTTAACT TCGATCCGATCGACAAGAATCAGATCCAGC TGTTCAATCTGGAATCTTCCAAAATCGAAG TTATCCTGAAGAATGCTATCGTATACAACT

              241               270 271               300 301               330 331              360
Original_Seq37   CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Substitute_Seq37 CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Amended_Seq37    CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG
Fig2_'975_App    CTATGTACGAAAACTTCTCCACCTCCTTCT GGATCCGTATCCCGAAATACTTCAACTCCA TCTCTCTGAACAATGAATACACCATCATCA ACTGCATGGAAAACAATTCTGGTTGGAAAG

              361               390 391               420 421               450 451              480
Original_Seq37   TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Substitute_Seq37 TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Amended_Seq37    TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT
Fig2_'975_App    TATCTCTGAACTACGGTGAAATCATCTGGA CTCTGCAGGACACTCAGGAAATCAAACAGC GTGTTGTATTCAAATACTCTCAGATGATCA ACATCTCTGACTACATCAATCGCTGGATCT

              481               510 511               540 541               570 571              600
Original_Seq37   TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGTTCTAATAACATCATGTTCA
Substitute_Seq37 TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGTTCTAATAACATCATGTTCA
Amended_Seq37    TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGTTCTAATAACATCATGTTCA
Fig2_'975_App    TCGTTACCATCACCAACAATCGTCTGAATA ACTCCAAAATCTACATCAACGCCGTCTGA TCGACCAGAAACCGATCTCCAATCTGGGTA ACATCCACGTTCTAATAACATCATGTTCA

              601               630 631               660 661               690 691              720
Original_Seq37   AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Substitute_Seq37 AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Amended_Seq37    AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA
Fig2_'975_App    AACTGGACGGTTGTCGTGACACTCACCGCT ACATCTGGATCAAATACTTCAATCTGTTCG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACCTGTACGACAACCAGTCCAATTCTGGTA

              721               750 751               780 781               810 811              840
Original_Seq37   TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Substitute_Seq37 TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Amended_Seq37    TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC
Fig2_'975_App    TCCTGAAAGACTTCTGGGGTGACTACCTGC AGTACGACAAACCGTACTACATGCTGAATC TGTACGATCCGAACAAATACGTTGACGTCA ACAATGTAGGTATCCGCGGTTACATGTACC

              841               870 871               900 901               930 931              960
Original_Seq37   TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATGGTTCGCA
Substitute_Seq37 TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA
Amended_Seq37    TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA
Fig2_'975_App    TGAAAGGTCCGCGTGGTTCTGTTATGACTA CCAACATCTACCTGAACTCTTCCCTGTACC GTGGTACCAAATTCATCATCAAGAAATACG CGTCTGGTAACAAGGACAATATCGTTCGCA

              961               990 991               1020 1021              1050 1051             1080
Original_Seq37   ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Substitute_Seq37 ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Amended_Seq37    ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Fig2_'975_App    ACAATGATCGTGTATACATCAATGTTGTAG TTAAGAACAAAGAATACCGTCTGGCTACCA ATGCTTCTCAGGCTGGTGTAGAAAAGATCT TGTCTGCTCTGGAAATCCCGGACGTTGGTA

              1081              1110 1111              1140 1141              1170 1171             1200
Original_Seq37   ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Substitute_Seq37 ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Amended_Seq37    ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA
Fig2_'975_App    ATCTGTCTCAGGTAGTTGTAATGAAATCCA AGAACGACCAGGGTATCACTAACAAATGCA AAATGAATCTGCAGGACAACAATGGTAACG ATATCGGTTTCATCGGTTTCCACCAGTTCA

              1201              1230 1231              1260 1261              1290 1291             1320
Original_Seq37   ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Substitute_Seq37 ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Amended_Seq37    ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC
Fig2_'975_App    ACAATATCGCTAAACTGGTTGCTTCCAACT GGTACAATCGTCAGATCGAACGTTCCTCTC GCACTCTGGGTTGCTCTTGGGAGTTCATCC CGGTTGATGACGGTTGGGGTGAACGTCCGC

              1321         1338
Original_Seq37   TGTAACCCGGGAAAGCTT
Substitute_Seq37 TGTAACCCGGGAAAGCTT
Amended_Seq37    TGTAACCCGGGAAAGCTT
Fig2_'975_App    TGTAACCCGGGAAAGCTT
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ALIGNMENT 3: SEQ ID NO:39

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                    1                 30 31                60 61                90 91               120
Original_Seq39      ATGGCTTTCAACAAATACAATTCCGAAATC CTGAACAATATCATCCTGAACCTGCGTTAC AAAGACAACAATCTGATCGATCTGTCTGGT TACGGTGCTAAAGTTGAAGTATACGACGGT
Substitute_Seq39    ATGGCCGCCAACAAATACAATTCCGAAATC CTGAACAATATCATCCTGAACCTGCGTTAC AAAGACAACAATCTGATCGATCTGTCTGGT TACGGTGCTAAAGTTGAAGTATACGACGGT
Amended_Seq39       ATGGCTTTCAACAAATACAATTCCGAAATC CTGAACAATATCATCCTGAACCTGCGTTAC AAAGACAACAATCTGATCGATCTGTCTGGT TACGGTGCTAAAGTTGAAGTATACGACGGT
Fig4_'975_App       ATGGCTTTCAACAAATACAATTCCGAAATC CTGAACAATATCATCCTGAACCTGCGTTAC AAAGACAACAATCTGATCGATCTGTCTGGT TACGGTGCTAAAGTTGAAGTATACGACGGT

                    121               150 151              180 181              210 211              240
Original_Seq39      GTTGAACTGAATGACAAGAACCAGTTCAAA CTGACCTCTTCCGCTAACTCTAAGATCCGT GTTACTCAGAATCAGAACATCATCTTCAAC TCCGTATTCCTGGACTTCTCTGTTTCCTTC
Substitute_Seq39    GTTGAACTGAATGACAAGAACCAGTTCAAA CTGACCTCTTCCGCTAACTCTAAGATCCGT GTTACTCAGAATCAGAACATCATCTTCAAC TCCGTATTCCTGGACTTCTCTGTTTCCTTC
Amended_Seq39       GTTGAACTGAATGACAAGAACCAGTTCAAA CTGACCTCTTCCGCTAACTCTAAGATCCGT GTTACTCAGAATCAGAACATCATCTTCAAC TCCGTATTCCTGGACTTCTCTGTTTCCTTC
Fig4_'975_App       GTTGAACTGAATGACAAGAACCAGTTCAAA CTGACCTCTTCCGCTAACTCTAAGATCCGT GTTACTCAGAATCAGAACATCATCTTCAAC TCCGTATTCCTGGACTTCTCTGTTTCCTTC

                    241               270 271              300 301              330 331              360
Original_Seq39      TGGATCCGTATCCCGAAATACAAGAACGAC GGTATCCAGAATTACATCCACAATGAATAC ACCATCATCAACTGCATGAAGAATAACTCT GGTTGGAAGATCTCCATCCGCGGTAACCGT
Substitute_Seq39    TGGATCCGTATCCCGAAATACAAGAACGAC GGTATCCAGAATTACATCCACAATGAATAC ACCATCATCAACTGCATGAAGAATAACTCT GGTTGGAAGATCTCCATCCGCGGTAACCGT
Amended_Seq39       TGGATCCGTATCCCGAAATACAAGAACGAC GGTATCCAGAATTACATCCACAATGAATAC ACCATCATCAACTGCATGAAGAATAACTCT GGTTGGAAGATCTCCATCCGCGGTAACCGT
Fig4_'975_App       TGGATCCGTATCCCGAAATACAAGAACGAC GGTATCCAGAATTACATCCACAATGAATAC ACCATCATCAACTGCATGAAGAATAACTCT GGTTGGAAGATCTCCATCCGCGGTAACCGT

                    361               390 391              420 421              450 451              480
Original_Seq39      ATCATCTGGACTCTGATCGATATCAACGGT AAGACCCAAATCTGTATTCTTCGAATACAAC ATCCGTGAAGACATCTCTGAATACATCAAT CGCTGGTTCTTCGTTACCATCACCAATAAC
Substitute_Seq39    ATCATCTGGACTCTGATCGATATCAACGGT AAGACCCAAATCTGTATTCTTCGAATACAAC ATCCGTGAAGACATCTCTGAATACATCAAT CGCTGGTTCTTCGTTACCATCACCAATAAC
Amended_Seq39       ATCATCTGGACTCTGATCGATATCAACGGT AAGACCCAAATCTGTATTCTTCGAATACAAC ATCCGTGAAGACATCTCTGAATACATCAAT CGCTGGTTCTTCGTTACCATCACCAATAAC
Fig4_'975_App       ATCATCTGGACTCTGATCGATATCAACGGT AAGACCCAAATCTGTATTCTTCGAATACAAC ATCCGTGAAGACATCTCTGAATACATCAAT CGCTGGTTCTTCGTTACCATCACCAATAAC

                    481               510 511              540 541              570 571              600
Original_Seq39      CTGAACAATGCTAAAATCTACATCAACGGT AAACTGGAATCTAATACCGACATCAAAGAC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCTTCAAACTGGACGGTGACATCGATCGT
Substitute_Seq39    CTGAACAATGCTAAAATCTACATCAACGGT AAACTGGAATCTAATACCGACATCAAAGAC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCTTCAAACTGGACGGTGACATCGATCGT
Amended_Seq39       CTGAACAATGCTAAAATCTACATCAACGGT AAACTGGAATCTAATACCGACATCAAAGAC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCTTCAAACTGGACGGTGACATCGATCGT
Fig4_'975_App       CTGAACAATGCTAAAATCTACATCAACGGT AAACTGGAATCTAATACCGACATCAAAGAC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCTTCAAACTGGACGGTGACATCGATCGT

                    601               630 631              660 661              690 691              720
Original_Seq39      ACCCAGTTCATCTGGATGAAATACTTCTCC ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCGAAGAACGGTACAAGATCCAGTCTTAC TCCGAATACCTGAAAGACTTCTGGGGTAAT
Substitute_Seq39    ACCCAGTTCATCTGGATGAAATACTTCTCC ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCGAAGAACGGTACAAGATCCAGTCTTAC TCCGAATACCTGAAAGACTTCTGGGGTAAT
Amended_Seq39       ACCCAGTTCATCTGGATGAAATACTTCTCC ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCGAAGAACGGTACAAGATCCAGTCTTAC TCCGAATACCTGAAAGACTTCTGGGGTAAT
Fig4_'975_App       ACCCAGTTCATCTGGATGAAATACTTCTCC ATCTTCAACACCGAACTGTCTCAGTCCAAT ATCGAAGAACGGTACAAGATCCAGTCTTAC TCCGAATACCTGAAAGACTTCTGGGGTAAT

                    721               750 751              780 781              810 811              840
Original_Seq39      CCGCTGATGTACAACAAAGAATACTATATG TTCAATGCTGGTAACAAGAACTCTTACATC AAACTGAAGAAAGACTCTCCGGTTGGTGAA GTCCTGACTCGTTCCAAATACAACCAGAAC
Substitute_Seq39    CCGCTGATGTACAACAAAGAATACTATATG TTCAATGCTGGTAACAAGAACTCTTACATC AAACTGAAGAAAGACTCTCCGGTTGGTGAA ATCCTGACTCGTTCCAAATACAACCAGAAC
Amended_Seq39       CCGCTGATGTACAACAAAGAATACTATATG TTCAATGCTGGTAACAAGAACTCTTACATC AAACTGAAGAAAGACTCTCCGGTTGGTGAA ATCCTGACTCGTTCCAAATACAACCAGAAC
Fig4_'975_App       CCGCTGATGTACAACAAAGAATACTATATG TTCAATGCTGGTAACAAGAACTCTTACATC AAACTGAAGAAAGACTCTCCGGTTGGTGAA ATCCTGACTCGTTCCAAATACAACCAGAAC

                    841               870 871              900 901              930 931              960
Original_Seq39      TCTAAATACATCAACTACCGCGACCTGTAC ATCGGTGAAAAGTTCATCATCCGTCGCAAA TCTAACTCTCAGTCCATCAATGAGGACATC GTACGTAAAGAAGACTACATCTACCTGGAC
Substitute_Seq39    TCTAAATACATCAACTACCGCGACCTGTAC ATCGGTGAAAAGTTCATCATCCGTCGCAAA TCTAACTCTCAGTCCATCAATGATGACATC GTACGTAAAGAAGACTACATCTACCTGGAC
Amended_Seq39       TCTAAATACATCAACTACCGCGACCTGTAC ATCGGTGAAAAGTTCATCATCCGTCGCAAA TCTAACTCTCAGTCCATCAATGATGACATC GTACGTAAAGAAGACTACATCTACCTGGAC
Fig4_'975_App       TCTAAATACATCAACTACCGCGACCTGTAC ATCGGTGAAAAGTTCATCATCCGTCGCAAA TCTAACTCTCAGTCCATCAATGATGACATC GTACGTAAAGAAGACTACATCTACCTGGAC

                    961               990 991             1020 1021            1050 1051            1080
Original_Seq39      TTCTTCAACCTGAATCAGTAATGGCGTGTA TACACCTACAAGTACTTCAAGAAAGAAGAA GAAAAGCTTTTCCTGGCTCCGATCTCTGAT TCCGACGAACTCTACAACACCATCCAGATC
Substitute_Seq39    TTCTTCAACCTGAATCAGTAATGGCGTGTA TACACCTACAAGTACTTCAAGAAAGAAGAA GAAAAGCTTTTCCTGGCTCCGATCTCTGAT TCCGACGAACTCTACAACACCATCCAGATC
Amended_Seq39       TTCTTCAACCTGAATCAGTAATGGCGTGTA TACACCTACAAGTACTTCAAGAAAGAAGAA GAAAAGCTTTTCCTGGCTCCGATCTCTGAT TCCGACGAACTCTACAACACCATCCAGATC
Fig4_'975_App       TTCTTCAACCTGAATCAGTAATGGCGTGTA TACACCTACAAGTACTTCAAGAAAGAAGAA GAAAAGCTTTTCCTGGCTCCGATCTCTGAT TCCGACGAACTCTACAACACCATCCAGATC

                    1081             1110 1111            1140 1141            1170 1171            1200
Original_Seq39      AAAGAATACGACGAACAGCCGACCTACTCT TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TCTACTGACGAAATCGGTCTGATCGGTATC CACCGTTTCTACGAATCTGGTATCGTATTC
Substitute_Seq39    AAAGAATACGACGAACAGCCGACCTACTCT TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TCTACTGACGAAATCGGTCTGATCGGTATC CACCGTTTCTACGAATCTGGTATCGTATTC
Amended_Seq39       AAAGAATACGACGAACAGCCGACCTACTCT TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TCTACTGACGAAATCGGTCTGATCGGTATC CACCGTTTCTACGAATCTGGTATCGTATTC
Fig4_'975_App       AAAGAATACGACGAACAGCCGACCTACTCT TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TCTACTGACGAAATCGGTCTGATCGGTATC CACCGTTTCTACGAATCTGGTATCGTATTC

                    1201             1230 1231            1260 1261            1290 1291            1320
Original_Seq39      GAAGAATACAAAGACTGCTTCTGCATCTCC AAATGGTACCTGAAGGAAGTTAAACGCAAA CCGTACAACCTGAAACTGGGTTGCAATTGG CAGTTCATCCCGAAAGACGAAGGTTGGACC
Substitute_Seq39    GAAGAATACAAAGACTACTTCTGCATCTCC AAATGGTACCTGAAGGAAGTTAAACGCAAA CCGTACAACCTGAAACTGGGTTGCAATTGG CAGTTCATCCCGAAAGACGAAGGTTGGACC
Amended_Seq39       GAAGAATACAAAGACTACTTCTGCATCTCC AAATGGTACCTGAAGGAAGTTAAACGCAAA CCGTACAACCTGAAACTGGGTTGCAATTGG CAGTTCATCCCGAAAGACGAAGGTTGGACC
Fig4_'975_App       GAAGAATACAAAGACTACTTCTGCATCTCC AAATGGTACCTGAAGGAAGTTAAACGCAAA CCGTACAACCTGAAACTGGGTTGCAATTGG CAGTTCATCCCGAAAGACGAAGGTTGGACC

                    1321             1350 1351
Original_Seq39      GAATAGTAACCTCTAGAGTCGAGGCCTGCA G
Substitute_Seq39    GAATAGTAACCTCTAGAGTCGAGGCCTGCA G
Amended_Seq39       GAATAGTAACCTCTAGAGTCGAGGCCTGCA G
Fig4_'975_App       GAATAGTAACCTCTAGAGTCGAGGCCTGCA G
```

ALIGNMENT 4: SEQ ID NO:40

```
                 1                        30 31                         60 61                        90 91                        120
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    MPVTINNFNYNDPIDNNNIIMMEPPFARGT GRYYKAFKITDRIWIIPERYTFGYKPEDFN KSSGIFNRDVCEYYDPDYLNTNDKKNIFLQ TMIKLFNRIKSKPLGEKLLEMIINGIPYLG
```

```
                 121                      150 151                        180 181                       210 211                       240
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    DRRVPLEEFNTNIASVTVNKLISNPGEVER KKGIFANLIIFGPGPVLNENETIDIGIQNH PASREGFGGIMQMKFCPEYVSVFNNVQENK GASIFNRRGYFSDPALILMHELIHVLHGLY
```

```
                 241                      270 271                        300 301                       330 331                       360
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    GIKVDDLPIVPNEKKPPMQSTDAIQAEELY TPGGQDPSIITPSTDKSIYDKVLQNFRGIV DRLNKVLVCISDPNININIYKNKFKDKYKP VEDSEGKYSIDVESFDKLYKSLMPGFTETN
```

```
                 361                      390 391                        420 421                       450 451                       480
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    IAENYKIKTRASYFSDSLPPVKIKNLLDNE IYTIEEGFNISDKDMEKEYRGQNKAINKQA YEEISKEHLAVYKIQMCKSVKAPGICIDVD NEDLFPIADKNSPSDDLSKNERIEYNTQSN
```

```
                 481                      510 511                        540 541                       570 571                       600
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    YIENDFPINELILDTDLISKIELPSENTES LTDFNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SFFSMDYIKTANKVVEAGLFAGWVKQIVND
```

```
                 601                      630 631                        660 661                       690 691                       720
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAFEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQPYTIKEGMY
```

```
                 721                      750 751                        780 781                       810 811                       840
Original_Seq40   -----------------------------  ----------------------------  ----------------------------  ----------------------------
Substitute_Seq40 -----------------------------  ----------------------------  ----------------------------  ----------------------------
Amended_Seq40    -----------------------------  ----------------------------  ----------------------------  ----------------------------
Whelan_M81186    KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDFDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
```

```
                 841                      870 871                        900 901                       930 931                       960
Original_Seq40   ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Substitute_Seq40 ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Amended_Seq40    ------------FNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Whelan_M81186    SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQFK LTSSANSKIRVTQNQNIIFNSVFLDFSVSP WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
```

```
                 961                      990 991                        1020 1021                     1050 1051                     1080
Original_Seq40   GWKISIRGNRI WTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIPKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Substitute_Seq40 GWKISIRGNRI WTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIPKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Amended_Seq40    GWKISIRGNRI WTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIPKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Whelan_M81186    GWKISIRGNRI WTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIPKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
```

```
                 1081                    1110 1111                       1140 1141                     1170 1171                     1200
Original_Seq40   SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEG RVYTYKG PKKEEEKLFLAPISD
Substitute_Seq40 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEG RVYTYKG PKKEEEKLFLAPISD
Amended_Seq40    SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEG RVYTYKG PKKEEEKLFLAPISD
Whelan_M81186    SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI KLKKDSPVGEILTRSKYNQNSKYINYRDLY IGEKFIIRRKSNSQSINDDIVRKEDYIYLD FFNLNQEG RVYTYKG PKKEEEKLFLAPISD
```

```
                 1201                    1230 1231                       1260 1261                     1290 1291
Original_Seq40   SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYPCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Substitute_Seq40 SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYPCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Amended_Seq40    SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYPCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
Whelan_M81186    SDEPYNTIQIKEYDEQPTYSCQLLFKKDEE STDEIGLIGIHRFYESGIVFEEYKDYPCIS KWYLKEVKRKPYNLKLGCNWQFIPKDEGWT E
```

ALIGNMENT 5: SEQ ID NO:41

```
                    1                30 31                60 61                90 91               120
Original_Seq41      ------------------------------ ------------------------------ ------------------------------ ------------------------------
Substitute_Seq41    ------------------------------ ------------------------------ ------------------------------ ------------------------------
Amended_Seq41       ------------------------------ ------------------------------ ------------------------------ ------------------------------
Thompson_X52066     MQFVNKQFNYKDPVNGVDIAYIKIPNVGQM QPVKAFKIHNKIWVIPERDTFTNPEEGDLN PPPEAKQVPVSYYDSTYLSTDNEKDNYLKG VTKLFERIYSTDLGRMLLTSIVRGIPFWGG


                    121              150 151              180 181              210 211              240
Original_Seq41      ------------------------------ ------------------------------ ------------------------------ ------------------------------
Substitute_Seq41    ------------------------------ ------------------------------ ------------------------------ ------------------------------
Amended_Seq41       ------------------------------ ------------------------------ ------------------------------ ------------------------------
Thompson_X52066     STIDTELKVIDTNCINVIQPDGSYRSEELN LVIIGPSADIIQPECKSFGHEVLNLTRNGY GSTQYIRFSPDFTPGFEESLEVDTNPLLGA GKFATDPAVTLAHELIHAGHRLYGIAINPN


                    241              270 271              300 301              330 331              360
Original_Seq41      ------------------------------ ------------------------------ ------------------------------ ------------------------------
Substitute_Seq41    ------------------------------ ------------------------------ ------------------------------ ------------------------------
Amended_Seq41       ------------------------------ ------------------------------ ------------------------------ ------------------------------
Thompson_X52066     RVFKVNTNAYYEMSGLEVSPEELRTFGGHD AKFIDSLQENEPRLYYYNKPKDIASTLNKA KSIVGTTASLQYMKNVFKEKYLLSEDTSGK FSVDKLKFDKLYKMLTEIYTEDNFVKFPKV


                    361              390 391              420 421              450 451              480
Original_Seq41      ------------------------------ ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Substitute_Seq41    ------------------------------ ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Amended_Seq41       ------------------------------ ------------------------------ --------------------------AL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
Thompson_X52066     LNRKTYLNFDKAVFKINIVPKVNYTIYDGP NLRNTNLAANFNGQNTEINNMMNFTKLKNFT GLFEFYKLLCVRGIITSKTKSLDKGYNKAL NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE


                    481              510 511              540 541              570 571              600
Original_Seq41      ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Substitute_Seq41    ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Amended_Seq41       ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA
Thompson_X52066     ITSDTNIEAAEENISLDLIQQYYLTFNFDN EPENISIENLSSDIIGQLELMPNIERFPNG KKYELDKYTMFHYLRAQEFEHGKSRIALTN SVNEALLNPSRVYTFFSSDYVKKVNKATEA


                    601              630 631              660 661              690 691              720
Original_Seq41      AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Substitute_Seq41    AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Amended_Seq41       AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Thompson_X52066     AMPLGWVEQLVYDFTDETSEVSTTDKIADI TIIIPYIGPALNIGMLYKDDFVGALIFSG AVILLEFIPEIAIPVLGTFALVSYIANKVL TVQTIDNALSKRNEKWDEVYKYIVTNWLAK


                    721              750 751              780 781              810 811              840
Original_Seq41      VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Substitute_Seq41    VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Amended_Seq41       VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNYGTLIGQVDRLKDK
Thompson_X52066     VNTQIDLIRKKMKEALENQAEATKAIINYQ YNQYTEEEKNNINFNIDDLSSKLNESINKA MININKFLNQCSVSYLMNSMIPYGVKRLED FDASLKDALLKYIRDNGTLIGQVDRLKDK


                    841              870 871              900 901              930 931              960
Original_Seq41      VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSFWIRIPKYFNSISLNN
Substitute_Seq41    VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSFWIRIPKYFNSISLNN
Amended_Seq41       VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSFWIRIPKYFNSISLNN
Thompson_X52066     VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI KNIINTSILNLRYESNHLIDLSRYASKINI GSKVNFDPIDKNQIQLFNLESSKIEVILKN AIVYNSMYENFSTSFWIRIPKYFNSISLNN


                    961              990 991             1020 1021            1050 1051            1080
Original_Seq41      EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Substitute_Seq41    EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Amended_Seq41       EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL
Thompson_X52066     EYTIINCMENNSGWKVSLNYGEIIWTLQDT QEIKQRVVFKYSQMINISDYINRWIFVTIT NNRLNNSKIYINGRLIDQKPISNLGNIHA SNNIMFKLDGCRDTHRYIWIKYFNLFDKEL


                    1081            1110 1111            1140 1141            1170 1171            1200
Original_Seq41      NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMILLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKYASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Substitute_Seq41    NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMILLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKYASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Amended_Seq41       NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMLNLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKYASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ
Thompson_X52066     NEKEIKDLYDNQSNSGILKDFWGDYLQYDK PYYMLNLYDPNKYVDVNNVGIRGYMYLKGP RGSVMTTNIYLNSSLYRGTKFIIKKYASGN KDNIVRNNDRVYINVVVKNKEYRLATNASQ


                    1201            1230 1231            1260 1261            1290 1297
Original_Seq41      AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGPHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Substitute_Seq41    AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGPHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Amended_Seq41       AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGPHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
Thompson_X52066     AGVEKILSALEIPDVGNLSQVVVMKSKNDQ GITNKCKMNLQDNNGNDIGFIGPHQFNNIA KLVASNWYNRQTERSSRTLGCSWEFIPVDD GWGERPL
```

ALIGNMENT 6: SEQ ID NO:42

```
                1              30 31                60 61                90 91               120
Original_Seq42  -------------------- -------------------- -------------------- --------------------
Substitute_Seq42 -------------------- -------------------- -------------------- --------------------
Amended_Seq42   -------------------- -------------------- -------------------- --------------------
Whelan_M81186   MPVTINNFNYNDPIDNNNIIMMEPPPFARGT GRYYKAFKITDRIWIIPERYTFGYKPEDPN KSSGIPNRDVCEYYDPDYLNTNDKKNIPLQ TMIKLFNRIKSKPLGEKLLEMIINGIPYLG


                121            150 151               180 181               210 211               240
Original_Seq42  -------------------- -------------------- -------------------- --------------------
Substitute_Seq42 -------------------- -------------------- -------------------- --------------------
Amended_Seq42   -------------------- -------------------- -------------------- --------------------
Whelan_M81186   DRRVPLEEFNTNIASVTVNKLISNPGEVER KKGIFANLIIFGPGPVLNENETIDIGIQNH FASREGFGGIMQMKFCPEYVSVPNNVQENK GASIFNRRGYFSDPALILMHELIHVLHGLY


                241            270 271               300 301               330 331               360
Original_Seq42  -------------------- -------------------- -------------------- --------------------
Substitute_Seq42 -------------------- -------------------- -------------------- --------------------
Amended_Seq42   -------------------- -------------------- -------------------- --------------------
Whelan_M81186   GIKVDDLPIVPNEKKPFMQSTDAIQAEELY TFGGQDPSIITPSTDKSIYDKVLQNPRGIV DRLNKVLVCISDPNININIYKNKPKDKYKF VEDSEGKYSIDVESFDKLYKSLMFGPTETN


                361            390 391               420 421               450 451               480
Original_Seq42  -------------------- -------------------- --------------------APGICIDVD NEDLFPIADKNSFSDDLSKNERIEYNTQSN
Substitute_Seq42 -------------------- -------------------- --------------------APGICIDVD NEDLFPIADKNSPDDLSKNERIEYNTQSN
Amended_Seq42   -------------------- -------------------- --------------------APGICIDVD NEDLFPIADKNSFSDDLSKNERIEYNTQSN
Whelan_M81186   IAENYKIKTRASYFSDSLPPVKIKNLLDNE IYTIEEGFNISDKDMEKEYRGQNKAINKQA YEEISKEHLAVYKIQMCKSVKAPGICIDVD NEDLFFIADKNSFSDDLSKNERIEYNTQSN


                481            510 511               540 541               570 571               600
Original_Seq42  YIENDFPINELILDTDLISKIELPSENTES LTDFNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Substitute_Seq42 YIENDFPINELILDTDLISKIELPSENTES LTDFNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Amended_Seq42   YIENDFPINELILDTDLISKIELPSENTES LTDFNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Whelan_M81186   YIENDFPINELILDTDLISKIELPSENTES LTDFNVDVPVYEKQPAIKKIFTDENTIPQY LYSQTFPLDIRDISLTSSFDDALLFSNKVY SPFSMDYIKTANKVVEAGLFAGWVKQIVND


                601            630 631               660 661               690 691               720
Original_Seq42  FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Substitute_Seq42 FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Amended_Seq42   FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Whelan_M81186   FVIEANKSNTMDKIADISLIVPYIGLALNV GNETAKGNFENAPEIAGASILLEFIPELLI PVVGAFLLESYIDNKNKIIKTIDNALTKRN EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY


                721            750 751               780 781               810 811               840
Original_Seq42  KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Substitute_Seq42 KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Amended_Seq42   KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Whelan_M81186   KALNYQAQALEEIIKYRYNIYSEKEKSNIN IDFNDINSKLNEGINQAIDNINNFINGCSV SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI DENKLYLIGSAEYEKSKVNKYLKTIMPFDL


                841            870 871               900 901               930 931               960
Original_Seq42  SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQPK LTSSANSKIRQTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Substitute_Seq42 SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQPK LTSSANSKIRQTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Amended_Seq42   SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQPK LTSSANSKIRQTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS
Whelan_M81186   SIYTNDTILIEMFNKYNSEILNNIILNLRY KDNNLIDLSGYGAKVEVYDGVELNDKNQPK LTSSANSKIRQTQNQNIIFNSVFLDFSVSF WIRIPKYKNDGIQNYIHNEYTIINCMKNNS


                961            990 991              1020 1021             1050 1051             1080
Original_Seq42  GWKISIRGRIIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Substitute_Seq42 GWKISIRGNRIIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Amended_Seq42   GWKISIRGNRIIWTLIDINGKTKSVFPEYN IREDISEYINRWFFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY
Whelan_M81186   GWKISIRGNRIIWTLIDINGKTKSVFPEYN IREDISEYINRWPFVTITNNLNNAKIYING KLESNTDIKDIREVIANGEIIFKLDGDIDR TQFIWMKYFSIFNTELSQSNIEERYKIQSY


                1081          1110 1111             1140 1141             1170 1171             1200
Original_Seq42  SEYLKDFWGNPLMYNKEYYMFNAGNKNSYS IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEEKLFLAPIS
Substitute_Seq42 SEYLKDFWGNPLMYNKEYYMFNAGNKNSYS IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEEKLFLAPIS
Amended_Seq42   SEYLKDFWGNPLMYNKEYYMFNAGNKNSYS IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEEKLFLAPIS
Whelan_M81186   SEYLKDFWGNPLMYNKEYYMFNAGNKNSYS IKLKKDSPVGEILTRSKYNQNSKYINYRDL YIGEKFIIRRKSNSQSINDDIVRKEDYIYL DFFNLNQEWRVYTYKYFKKEEEKLFLAPIS


                1201          1230 1231             1260 1261             1290 1292
Original_Seq42  DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRFYESGIVFEEMKDUPCI SMWYLMEVKRKPYNLKLGCNWQFIPKDEGW TE
Substitute_Seq42 DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRFYESGIVFEEMKDUPCI SMWYLMEVKRKPYNLKLGCNWQFIPKDEGW TE
Amended_Seq42   DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRFYESGIVFEEMKDUPCI SMWYLMEVKRKPYNLKLGCNWQFIPKDEGW TE
Whelan_M81186   DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE ESTDEIGLIGIHRFYESGIVFEEMKDUPCI SMWYLMEVKRKPYNLKLGCNWQFIPKDEGW TE
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